Special Issue

Genomewide SNP Identification and Use for Resolving Population Structure and GWAS of Traits of Interest Volume II

Message from the Guest Editors

With the merging of methodologies for making reduced-representation/resequencing libraries, RNAseq, next-generation sequencing and bioinformatic approaches have recently emerged for identifying genome-wide SNPs and insertions/deletions (InDELs) for resolving population structure, along with genome-wide association studies (GWAS), QTL/eQTL mapping, and bulk segregant analysis, which can be used to identify genomic regions of interest. In Volume II, we expand the scope of functional genomics involving RNAseq and qRT-PCR validations targeting mapped traits of interest.

The purpose of this Special Issue is to publish high-quality research papers as well as review articles addressing recent studies involving SNP mining, resolving population structures, haplotype networking, and GWAS as emerging tools for plant breeding and ecology research. Original, high-quality contributions that have not yet been published or that are not currently under review by other journals or peer-reviewed conferences are sought.

Guest Editors

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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